



Sequence Listing

<110> Lasky, Laurence A.
Dowbenko, Donald J.

<120> Tyrosine Phosphorylated Cleavage Furrow-Associated
Proteins (PSTPIPs)

<130> P1066P2

<140> US 09/068,377

<141> 1998-05-08

<150> PCT/US98/01774

<151> 1998-01-30

<150> US 08/938,830

<151> 1997-09-29

<150> US 60/104,589

<151> 1997-02-07

<160> 73

<210> 1

<211> 415

<212> PRT

<213> Mus Musculus

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				20					25					30

Asp	Gly	Arg	Lys	Met	Cys	Lys	Asp	Val	Glu	Glu	Leu	Leu	Arg	Gln
				35					40					45

Arg	Ala	Gln	Ala	Glu	Glu	Arg	Tyr	Gly	Lys	Glu	Leu	Val	Gln	Ile
				50					55					60

Ala	Arg	Lys	Ala	Gly	Gly	Gln	Thr	Glu	Met	Asn	Ser	Leu	Arg	Thr
				65					70					75

Ser	Phe	Asp	Ser	Leu	Lys	Gln	Gln	Thr	Glu	Asn	Val	Gly	Ser	Ala
				80					85					90

His	Ile	Gln	Leu	Ala	Leu	Ala	Leu	Arg	Glu	Glu	Leu	Arg	Ser	Leu
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Glu	Glu	Phe	Arg	Glu	Arg	Gln	Lys	Glu	Gln	Arg	Lys	Lys	Tyr	Glu
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Ala	Ile	Met	Asp	Arg	Val	Gln	Lys	Ser	Lys	Leu	Ser	Leu	Tyr	Lys
				125					130					135

Lys	Thr	Met	Glu	Ser	Lys	Lys	Ala	Tyr	Asp	Gln	Lys	Cys	Arg	Asp	
				140					145					150	
Ala	Asp	Asp	Ala	Glu	Gln	Ala	Phe	Glu	Arg	Val	Ser	Ala	Asn	Gly	
				155					160					165	
His	Gln	Lys	Gln	Val	Glu	Lys	Ser	Gln	Asn	Lys	Ala	Lys	Gln	Cys	
				170					175					180	
Lys	Glu	Ser	Ala	Thr	Glu	Ala	Glu	Arg	Val	Tyr	Arg	Gln	Asn	Ile	
				185					190					195	
Glu	Gln	Leu	Glu	Arg	Ala	Arg	Thr	Glu	Trp	Glu	Gln	Glu	His	Arg	
				200					205					210	
Thr	Thr	Cys	Glu	Ala	Phe	Gln	Leu	Gln	Glu	Phe	Asp	Arg	Leu	Thr	
				215					220					225	
Ile	Leu	Arg	Asn	Ala	Leu	Trp	Val	His	Cys	Asn	Gln	Leu	Ser	Met	
				230					235					240	
Gln	Cys	Val	Lys	Asp	Asp	Glu	Leu	Tyr	Glu	Glu	Val	Arg	Leu	Thr	
				245					250					255	
Leu	Glu	Gly	Cys	Asp	Val	Glu	Gly	Asp	Ile	Asn	Gly	Phe	Ile	Gln	
				260					265					270	
Ser	Lys	Ser	Thr	Gly	Arg	Glu	Pro	Pro	Ala	Pro	Val	Pro	Tyr	Gln	
				275					280					285	
Asn	Tyr	Tyr	Asp	Arg	Glu	Val	Thr	Pro	Leu	Ile	Gly	Ser	Pro	Ser	
				290					295					300	
Ile	Gln	Pro	Ser	Cys	Gly	Val	Ile	Lys	Arg	Phe	Ser	Gly	Leu	Leu	
				305					310					315	
His	Gly	Ser	Pro	Lys	Thr	Thr	Pro	Ser	Ala	Pro	Ala	Ala	Ser	Thr	
				320					325					330	
Glu	Thr	Leu	Thr	Pro	Thr	Pro	Glu	Arg	Asn	Glu	Leu	Val	Tyr	Ala	
				335					340					345	
Ser	Ile	Glu	Val	Gln	Ala	Thr	Gln	Gly	Asn	Leu	Asn	Ser	Ser	Ala	
				350					355					360	
Gln	Asp	Tyr	Arg	Ala	Leu	Tyr	Asp	Tyr	Thr	Ala	Gln	Asn	Ser	Asp	
				365					370					375	
Glu	Leu	Asp	Ile	Ser	Ala	Gly	Asp	Ile	Leu	Ala	Val	Ile	Leu	Glu	
				380					385					390	
Gly	Glu	Asp	Gly	Trp	Trp	Thr	Val	Glu	Arg	Asn	Gly	Gln	Arg	Gly	
				395					400					405	
Phe	Val	Pro	Gly	Ser	Tyr	Leu	Glu	Lys	Leu						
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<212> DNA
<213> Mus Musculus

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attgctgata gctcattgtc cttcactttc actaacagta gcaacggtcc 150
gaacctcata acaactcaaa caaattctca agcgctttca caaccaattg 200
cctcctctaa cgttcatgat aacttcatga ataataaat cacggctagt 250
aaaattgatg atggtaataa ttcaaaacca ctgtcacctg gttggacgga 300
ccaaactgcg tataacgcgt ttggaatcac tacagggatg tttataacca 350
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ccaaacccaa aaaaagaggg tgggtcgacc cacgcgtccg gtccttcct 450
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tcctccggca gttgcctctg gcttgtggct gccttctgag cgtttcagac 550
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caagaaggca tatgaccaga agtgcaggga tgcagatgat gctgagcagg 1150
ccttcgagcg tgtgagtgcc aatggccacc agaagcaagt agaaaagagc 1200
cagaacaaag ccaagcagtg caaggagtca gccacagagg cagaaagagt 1250
gtacaggcaa aatatcgaac aactggagag agcgaggacc gagtgggagc 1300

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atacctccgc cctgactgtg aggtcaggac tgtttctttc catcaccgcc 2000
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<210> 3

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<212> PRT

<213> Mus Musculus

<400> 3

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Ala Gly Asp Ile Leu Ala Val Ile Leu Glu Gly Glu Asp Gly Trp
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Trp Thr Val Glu Arg Asn Gly Gln Arg Gly Phe Val Pro Gly Ser
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Tyr Leu Arg

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<211> 50

<212> PRT

<213> Homo sapien

<400> 4

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Val	Asn	Glu	Val	Ile	Glu	Ile	Leu	Ile	Glu	Asp	Ser	Ser	Gly	Trp
			20						25					30
Trp	Lys	Gly	Arg	Leu	His	Gly	Gln	Glu	Gly	Leu	Phe	Pro	Gly	Asn
			35						40					45
Tyr	Val	Glu	Lys	Ile										
				50										

<210> 5
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 <213> Homo sapien

Leu	Tyr	Asp	Tyr	Gln	Glu	Lys	Ser	Pro	Arg	Glu	Val	Thr	Met	Lys
1				5					10					15
Lys	Gly	Asp	Ile	Leu	Thr	Leu	Leu	Asn	Ser	Thr	Asn	Lys	Asp	Trp
			20						25					30
Trp	Lys	Val	Glu	Val	Asn	Asp	Arg	Gln	Gly	Phe	Val	Pro	Ala	Ala
			35						40					45
Tyr	Val	Lys	Lys	Leu										
				50										

<210> 6
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 <212> PRT
 <213> Homo sapien

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Pro	Asp	Asp	Ile	Ile	Thr	Asp	Ile	Glu	Met	Val	Asp	Glu	Gly	Trp
			20						25					30
Trp	Arg	Gly	Gln	Cys	Arg	Gly	His	Phe	Gly	Leu	Phe	Pro	Ala	Asn
			35						40					45
Tyr	Val	Lys	Leu	Leu										
				50										

<210> 7
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 <213> Homo sapien

Leu	Tyr	Asp	Tyr	Gln	Ala	Ala	Gly	Asp	Asp	Glu	Ile	Ser	Phe	Asp
1				5					10					15

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20 25 30

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35 40 45

Tyr Val Glu

<210> 8

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<212> PRT

<213> Artificial Sequence

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<223> Amino acid epitope tag

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<210> 9

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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cgcgatcca ccatgatggc ccagctgcag ttc 33

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<213> Artificial Sequence

<220>

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gtacgctcg actcacttgt catcgctcgtc cttgtagtcg agctt 45

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 11

tgcctttctc tccacagg 18

<210> 12

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 12

ctccttgagg ttctactagt gggggctggg gtcctg 36

<210> 13

<211> 39

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 17

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gcgtttggaa tcactac 17

<210> 15

<211> 41

<212> DNA

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<210> 16

<211> 37

<212> DNA

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gtacgcgtcg accgcactct acgactacac tgcacag 37

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<400> 17

ctctggcgaa gaagtcc 17

<210> 18

<211> 32

<212> DNA

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<400> 18

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<211> 38

<212> DNA

<213> Artificial Sequence

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<400> 19

gatacctcgag ttacacccgt gtccactctg ctggagga 38

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<213> Artificial Sequence

<220>

<223> Synthetic oligopeptide

<400> 20

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Pro	Ala	Glu	Trp	Thr
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<211> 19

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<220>

<223> Synthetic oligopeptide

<400> 21

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Pro	Ser	Ala	Trp
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 <212> PRT
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Pro Ser Glu Trp Thr
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<210> 23
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 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 23
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 1 5 10 15

Pro Met Ala Asp Thr
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<210> 24
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 24
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<210> 25
 <211> 36
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 25
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<210> 26
 <211> 907
 <212> PRT
 <213> Saccharomyces Pombe

<400> 26

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Ile	Asp	Glu	Phe	Tyr	Ala	Lys	Arg	Ala	Ser	Ile	Glu	Arg	Glu	Tyr	35	40	45	
Ala	Ser	Lys	Leu	Gln	Glu	Leu	Ala	Ala	Ser	Ser	Ala	Asp	Ile	Pro	50	55	60	
Glu	Val	Gly	Ser	Thr	Leu	Asn	Asn	Ile	Leu	Ser	Met	Arg	Thr	Glu	65	70	75	
Thr	Gly	Ser	Met	Ala	Lys	Ala	His	Glu	Glu	Val	Ser	Gln	Gln	Ile	80	85	90	
Asn	Thr	Glu	Leu	Arg	Asn	Lys	Ile	Arg	Glu	Tyr	Ile	Asp	Gln	Thr	95	100	105	
Glu	Gln	Gln	Lys	Val	Val	Ala	Ala	Asn	Ala	Ile	Glu	Glu	Leu	Tyr	110	115	120	
Gln	Lys	Lys	Thr	Ala	Leu	Glu	Ile	Asp	Leu	Ser	Glu	Lys	Lys	Asp	125	130	135	
Ala	Tyr	Glu	Tyr	Ser	Cys	Asn	Lys	Leu	Asn	Ser	Tyr	Met	Arg	Gln	140	145	150	
Thr	Lys	Lys	Met	Thr	Gly	Arg	Glu	Leu	Asp	Lys	Tyr	Asn	Leu	Lys	155	160	165	
Ile	Arg	Gln	Ala	Ala	Leu	Ala	Val	Lys	Lys	Met	Asp	Ala	Glu	Tyr	170	175	180	
Arg	Glu	Thr	Asn	Glu	Leu	Leu	Leu	Thr	Val	Thr	Arg	Glu	Trp	Ile	185	190	195	
Asp	Arg	Trp	Thr	Glu	Val	Cys	Asp	Ala	Phe	Gln	His	Ile	Glu	Glu	200	205	210	
Tyr	Arg	Leu	Glu	Phe	Leu	Lys	Thr	Asn	Met	Trp	Ala	Tyr	Ala	Asn	215	220	225	
Ile	Ile	Ser	Thr	Ala	Cys	Val	Lys	Asp	Asp	Glu	Ser	Cys	Glu	Lys	230	235	240	
Ile	Arg	Leu	Thr	Leu	Glu	Asn	Thr	Asn	Ile	Asp	Glu	Asp	Ile	Thr	245	250	255	
Gln	Met	Ile	Gln	Asn	Glu	Gly	Thr	Gly	Thr	Thr	Ile	Pro	Pro	Leu	260	265	270	
Pro	Glu	Phe	Asn	Asp	Tyr	Phe	Lys	Glu	Asn	Gly	Leu	Asn	Tyr	Asp				

275					280					285				
Ile	Asp	Gln	Leu	Ile	Ser	Lys	Ala	Pro	Ser	Tyr	Pro	Tyr	Ser	Ser
				290					295					300
Ser	Arg	Pro	Ser	Ala	Ser	Ala	Ser	Leu	Ala	Ser	Ser	Pro	Thr	Arg
				305					310					315
Ser	Ala	Phe	Arg	Pro	Lys	Thr	Ser	Glu	Thr	Val	Ser	Ser	Glu	Val
				320					325					330
Val	Ser	Ser	Pro	Pro	Thr	Ser	Pro	Leu	His	Ser	Pro	Val	Lys	Pro
				335					340					345
Val	Ser	Asn	Glu	Gln	Val	Glu	Gln	Val	Thr	Glu	Val	Glu	Leu	Ser
				350					355					360
Ile	Pro	Val	Pro	Ser	Ile	Gln	Glu	Ala	Glu	Ser	Gln	Lys	Pro	Val
				365					370					375
Leu	Thr	Gly	Ser	Ser	Met	Arg	Arg	Pro	Ser	Val	Thr	Ser	Pro	Thr
				380					385					390
Phe	Glu	Val	Ala	Ala	Arg	Pro	Leu	Thr	Ser	Met	Asp	Val	Arg	Ser
				395					400					405
Ser	His	Asn	Ala	Glu	Thr	Glu	Val	Gln	Ala	Ile	Pro	Ala	Ala	Thr
				410					415					420
Asp	Ile	Ser	Pro	Glu	Val	Lys	Glu	Gly	Lys	Asn	Ser	Glu	Asn	Ala
				425					430					435
Ile	Thr	Lys	Asp	Asn	Asp	Asp	Ile	Ile	Leu	Ser	Ser	Gln	Leu	Gln
				440					445					450
Pro	Thr	Ala	Thr	Gly	Ser	Arg	Ser	Ser	Arg	Leu	Ser	Phe	Ser	Arg
				455					460					465
His	Gly	His	Gly	Ser	Gln	Thr	Ser	Leu	Gly	Ser	Ile	Lys	Arg	Lys
				470					475					480
Ser	Ile	Met	Glu	Arg	Met	Gly	Arg	Pro	Thr	Ser	Pro	Phe	Met	Gly
				485					490					495
Ser	Ser	Phe	Ser	Asn	Met	Gly	Ser	Arg	Ser	Thr	Ser	Pro	Thr	Lys
				500					505					510
Glu	Gly	Phe	Ala	Ser	Asn	Gln	His	Ala	Thr	Gly	Ala	Ser	Val	Gln
				515					520					525
Ser	Asp	Glu	Leu	Glu	Asp	Ile	Asp	Pro	Arg	Ala	Asn	Val	Val	Leu
				530					535					540
Asn	Val	Gly	Pro	Asn	Met	Leu	Ser	Val	Gly	Glu	Ala	Pro	Val	Glu
				545					550					555
Ser	Thr	Ser	Lys	Glu	Glu	Asp	Lys	Asp	Val	Pro	Asp	Pro	Ile	Ala

560										565				570			
Asn	Ala	Met	Ala	Glu	Leu	Ser	Ser	Ser	Met	Arg	Arg	Arg	Gln	Ser			
				575					580					585			
Thr	Ser	Val	Asp	Asp	Glu	Ala	Pro	Val	Ser	Leu	Ser	Lys	Thr	Ser			
				590					595					600			
Ser	Ser	Thr	Arg	Leu	Asn	Gly	Leu	Gly	Tyr	His	Ser	Arg	Asn	Thr			
				605					610					615			
Ser	Ile	Ala	Ser	Asp	Ile	Asp	Gly	Val	Pro	Lys	Lys	Ser	Thr	Leu			
				620					625					630			
Gly	Ala	Pro	Pro	Ala	Ala	His	Thr	Ser	Ala	Gln	Met	Gln	Arg	Met			
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Ser	Asn	Ser	Phe	Ala	Ser	Gln	Thr	Lys	Gln	Val	Phe	Gly	Glu	Gln			
				650					655					660			
Arg	Thr	Glu	Asn	Ser	Ala	Arg	Glu	Ser	Leu	Arg	His	Ser	Arg	Ser			
				665					670					675			
Asn	Met	Ser	Arg	Ser	Pro	Ser	Pro	Met	Leu	Ser	Arg	Arg	Ser	Ser			
				680					685					690			
Thr	Leu	Arg	Pro	Ser	Phe	Glu	Arg	Ser	Ala	Ser	Ser	Leu	Ser	Val			
				695					700					705			
Arg	Gln	Ser	Asp	Val	Val	Ser	Pro	Ala	Pro	Ser	Thr	Arg	Ala	Arg			
				710					715					720			
Gly	Gln	Ser	Val	Ser	Gly	Gln	Gln	Arg	Pro	Ser	Ser	Ser	Met	Ser			
				725					730					735			
Leu	Tyr	Gly	Glu	Tyr	Asn	Lys	Ser	Gln	Pro	Gln	Leu	Ser	Met	Gln			
				740					745					750			
Arg	Ser	Val	Ser	Pro	Asn	Pro	Leu	Gly	Pro	Asn	Arg	Arg	Ser	Ser			
				755					760					765			
Ser	Val	Leu	Gln	Ser	Gln	Lys	Ser	Thr	Ser	Ser	Asn	Thr	Ser	Asn			
				770					775					780			
Arg	Asn	Asn	Gly	Gly	Tyr	Ser	Gly	Ser	Arg	Pro	Ser	Ser	Glu	Met			
				785					790					795			
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				800					805					810			
Ser	Gln	Arg	Ser	Thr	Ser	Arg	Ala	Arg	Ser	Pro	Glu	Pro	Thr	Asn			
				815					820					825			
Arg	Asn	Ser	Val	Gln	Ser	Lys	Asn	Val	Asp	Pro	Arg	Ala	Thr	Phe			
				830					835					840			
Thr	Ala	Glu	Gly	Glu	Pro	Ile	Leu	Gly	Tyr	Val	Ile	Ala	Leu	Tyr			

845					850					855				
Asp	Tyr	Gln	Ala	Gln	Ile	Pro	Glu	Glu	Ile	Ser	Phe	Gln	Lys	Gly
				860					865					870
Asp	Thr	Leu	Met	Val	Leu	Arg	Thr	Gln	Glu	Asp	Gly	Trp	Trp	Asp
				875					880					885
Gly	Glu	Ile	Ile	Asn	Val	Pro	Asn	Ser	Lys	Arg	Gly	Leu	Phe	Pro
				890					895					900
Ser	Asn	Phe	Val	Gln	Thr	Val								
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<210> 27
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Any amino acid

<400> 27
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<210> 28
 <211> 1613
 <212> DNA
 <213> Homo sapien

<400> 28
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 ctatagggct cgagcggccg cccgggcagg tctagaattc agcggccgct 150
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				20					25					30
Asp	Gly	Arg	Lys	Met	Cys	Lys	Asp	Met	Glu	Glu	Leu	Leu	Arg	Gln
				35					40					45
Arg	Ala	Gln	Ala	Glu	Glu	Arg	Tyr	Gly	Lys	Glu	Leu	Val	Gln	Ile

50					55					60				
Ala	Arg	Lys	Ala	Gly	Gly	Gln	Thr	Glu	Ile	Asn	Ser	Leu	Arg	Ala
				65					70					75
Ser	Phe	Asp	Ser	Leu	Lys	Gln	Gln	Met	Glu	Asn	Val	Gly	Ser	Ser
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His	Ile	Gln	Leu	Ala	Leu	Thr	Leu	Arg	Glu	Glu	Leu	Arg	Ser	Leu
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Glu	Glu	Phe	Arg	Glu	Arg	Gln	Lys	Glu	Gln	Arg	Lys	Lys	Gly	Met
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Ala	Val	Pro	Arg	Gln	Ser	Asp	Cys	Met	Glu	Val	Lys	Ser	Pro	Ser
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Trp	Glu	Tyr	Glu	Ala	Val	Met	Asp	Arg	Val	Gln	Lys	Ser	Lys	Leu
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Ser	Leu	Tyr	Lys	Lys	Ala	Met	Glu	Ser	Lys	Lys	Thr	Tyr	Glu	Gln
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Lys	Cys	Arg	Asp	Ala	Asp	Asp	Ala	Glu	Gln	Ala	Phe	Glu	Arg	Ile
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Ser	Ala	Asn	Gly	His	Gln	Lys	Gln	Val	Glu	Lys	Ser	Gln	Asn	Lys
				185					190					195
Ala	Arg	Gln	Cys	Lys	Asp	Ser	Ala	Thr	Glu	Ala	Glu	Arg	Val	Tyr
				200					205					210
Arg	Gln	Ser	Ile	Ala	Gln	Leu	Glu	Lys	Val	Arg	Ala	Glu	Trp	Glu
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Gln	Glu	His	Arg	Thr	Thr	Cys	Glu	Ala	Phe	Gln	Leu	Gln	Glu	Phe
				230					235					240
Asp	Arg	Leu	Thr	Ile	Leu	Arg	Asn	Ala	Leu	Trp	Val	His	Ser	Asn
				245					250					255
Gln	Leu	Ser	Met	Gln	Cys	Val	Lys	Asp	Asp	Glu	Leu	Tyr	Glu	Glu
				260					265					270
Val	Arg	Leu	Thr	Leu	Glu	Gly	Cys	Ser	Ile	Asp	Ala	Asp	Ile	Asp
				275					280					285
Ser	Phe	Ile	Gln	Ala	Lys	Ser	Thr	Gly	Thr	Glu	Pro	Pro	Arg	Phe
				290					295					300
Ser	Gly	Leu	Leu	His	Gly	Ser	Pro	Lys	Thr	Thr	Ser	Ser	Ala	Ser
				305					310					315
Ala	Gly	Ser	Thr	Glu	Thr	Leu	Thr	Pro	Thr	Pro	Glu	Arg	Asn	Glu
				320					325					330
Gly	Val	Tyr	Thr	Ala	Ile	Ala	Val	Gln	Glu	Ile	Gln	Gly	Asn	Pro

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Ala Ser Pro Ala	Gln Asp Tyr Arg Ala	Leu Tyr Asp Tyr Thr	Ala		
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Gln Asn Pro Asp	Glu Leu Asp Leu Ser	Ala Gly Asp Ile Leu	Glu		
	365	370	375		
Gly Glu Asp Gly	Trp Trp Thr Val Glu	Arg Asn Gly Gln Arg	Gly		
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Phe Val Pro Gly	Ser Tyr Leu Glu Lys	Leu			
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